SEQUENCE LISTING

<110> Michael Moore
      Yen Choo
      Aaron Klug

<120> ENGINEERED ZINC FINGER PROTEINS FOR REGULATION OF GENE EXPRESSION

<130> 8325-0038 (S38-US1)

<140> 10/572,886
<141> 2006-10-03

<150> PCT/US2004/030606
<151> 2004-09-17

<150> 60/504,502
<151> 2003-09-19

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<170> PatentIn version 3.3

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Thr Ser Ser Gly Leu Ser Arg
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      with target mammalian sequences

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<210> 20
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<212> PRT
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Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Asp Asn Arg Asp
            35   40   45

Arg Thr Lys His Thr Lys Ile His Thr Gly Gly Gln Arg Pro Tyr Ala
    50   55   60

Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Asp Arg Lys Thr Leu
65   70   75   80

Ile Glu His Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg
                85   90   95

Ile Cys Met Arg Asn Phe Ser Thr Ser Ser Gly Leu Ser Arg His Ile
            100   105   110

Arg Thr His Thr Gly Ser Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
            115   120   125

Arg Asn Phe Ser Arg Ser Asp His Leu Ser Glu His Ile Arg Thr His
    130   135   140

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc   180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc agatatacg cgttgacatt   240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata   300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc   360

9

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc   420

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atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca   600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg   660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc   720

aaaatcaacg ggactttcca aaatgtcgta caactccgc cccattgacg caaatgggcg   780

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ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc   900

gtttaaactt aagctgatcc actagtccag tgtggtggaa ttcgctagcg ccacc atg   958
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                                                                  1

gcc ccc aag aag aag agg aag gtg gga atc gat ggg gta ccc ttc cag   1006
Ala Pro Lys Lys Lys Arg Lys Val Gly Ile Asp Gly Val Pro Phe Gln
              5   10   15

tgt cga atc tgc atg cgt aac ttc agt cgt agt gac cac ctg agc cgg   1054
Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Ser Arg
         20   25   30

cac atc cgc acc cac aca ggc gag aag cct ttt gcc tgt gac att tgt   1102
His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys
         35   40   45

ggg agg aaa ttt gcc gac aac cgg gac cgc aca aag cat acc aag ata   1150
Gly Arg Lys Phe Ala Asp Asn Arg Asp Arg Thr Lys His Thr Lys Ile
50   55   60   65

cac acg ggc gga cag cgg ccg tac gca tgc cct gtc gag tcc tgc gat   1198
His Thr Gly Gly Gln Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp
                  70   75   80

cgc cgc ttt tct gac agg aag aca ctt atc gag cat atc cgc atc cac   1246
Arg Arg Phe Ser Asp Arg Lys Thr Leu Ile Glu His Ile Arg Ile His
              85   90   95

acc ggt cag aag ccc ttc cag tgt cga atc tgc atg cgt aac ttc agt   1294
Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser
             100   105   110

acc agc agc ggg ctg agc cgc cac atc cgc acc cac aca gga tct cag   1342
Thr Ser Ser Gly Leu Ser Arg His Ile Arg Thr His Thr Gly Ser Gln
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aag ccc ttc cag tgt cga atc tgc atg cgt aac ttc agt cgt agt gac   1390
Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp
130   135   140   145

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cac ctg agc gaa cac att cgc acc cac aca ggc gag aag cct ttt gcc       1438
His Leu Ser Glu His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala
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tgt gac att tgt ggg agg aaa ttt gcc acc agc agc gac cgc aca aag       1486
Cys Asp Ile Cys Gly Arg Lys Phe Ala Thr Ser Ser Asp Arg Thr Lys
            165             170                 175

cat acc aag ata cac ctg cgc caa aaa gat gcg gcc cgg gga tcc ggc       1534
His Thr Lys Ile His Leu Arg Gln Lys Asp Ala Ala Arg Gly Ser Gly
        180             185                 190

atg gat gct aag tca cta act gcc tgg tcc cgg aca ctg gtg acc ttc       1582
Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu Val Thr Phe
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aag gat gta ttt gtg gac ttc acc agg gag gag tgg aag ctg ctg gac       1630
Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp
210             215                 220                 225

act gct cag cag atc gtg tac aga aat gtg atg ctg gag aac tat aag       1678
Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys
                230             235                 240

aac ctg gtt tcc ttg ggt tat cag ctt act aag cca gat gtg atc ctc       1726
Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu
            245             250                 255

cgg ttg gag aag gga gaa gag ccc tgg ctg gtg gag aga gaa att cac       1774
Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His
            260             265                 270

caa gag acc cat cct gat tca gag act gca ttt gaa atc aaa tca tca       1822
Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser
    275             280                 285

gtt gac tac aag gac gac gat gac aag taagcttctc gagtctagct            1869
Val Asp Tyr Lys Asp Asp Asp Asp Lys
290             295

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13

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<210>  39
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<400>  39
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<400>  52
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<210>  53
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<212>  PRT
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<220>
<223>  Zinc finger protein designed to bind to a target sequence in the rat
       phospholamban gene


<400>  53

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Phe Ser Thr Ser Ala Asp Leu Thr Glu His Ile Arg Ile His Thr Gly
            20                  25                  30


Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Ala Ser
            35                  40                  45


Ala Asn Leu Ser Arg His Ile Arg Thr His Thr Gly Gly Glu Arg Pro
    50                  55                  60


Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Ala Leu
65                  70                  75                  80


Ser Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
                85                  90                  95
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19

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Ile Cys Gly Arg Lys Phe Ala Asp Arg Ser Thr Arg Thr Lys His Thr
            100                 105                 110

Lys Ile His Thr Gly Ser Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
        115                 120                 125

Arg Asn Phe Ser Arg Ser Asp Val Leu Ser Ala His Ile Arg Thr His
    130                 135                 140

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Lys Lys Phe Ala
145                 150                 155                 160

Asp Arg Ser Asn Arg Ile Lys His Thr Lys Ile His Leu Arg Gln Lys
            165                 170                 175

Asp Ala Ala Arg
            180
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